IN THE CLAIMS

This listing of the claims replaces all prior versions of the claims in the application.

Claims 1-2 (canceled)

Claim 3. (Previously presented) An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

- a.) a polypeptide comprising the amino acid sequence of SEQ ID NO:1,
- b) a polypeptide comprising an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:1,
- c) a fragment of a polypeptide having the amino acid sequence of SEQ ID NO:1, said fragment having cyclic nucleotide phosphodiesterase activity, and
- d) an immunogenic fragment of a polypeptide of at least 5 amino acids of the amino acid sequence of SEQ ID NO:1, said immunogenic fragment is used to make an antibody which specifically binds to an isolated polypeptide selected from the group consisting of a), b) and c).

Claims 4-5 (canceled)

Claim 6. (Original) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

Claim 7. (Original) A cell transformed with a recombinant polynucleotide of claim 6.

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Claim 8. (Previously presented) A method for producing a polypeptide encoded by the polynucleotide of claim 3, the method comprising:

- a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide of claim 3, and
- b) recovering the polypeptide so expressed.

Claims 9-10 (canceled)

Claim 11. (Previously presented) An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising the polynucleotide sequence of SEQ ID NO:2,
- b) a polynucleotide comprising a polynucleotide sequence at least 90% identical to the polynucleotide sequence of SEQ ID NO:2,
- c) a polynucleotide complementary to a polynucleotide of a),
- d) a polynucleotide complementary to a polynucleotide of b) and
- e) an RNA equivalent of a)-d).

Claim 12 (canceled)

Claim 13. (Original) A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.
- Claim 14. (Original) A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.
- Claim 15. (Original) A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:
 - a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
 - b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

Claims 16-19 (canceled)

Claim 20. (Withdrawn) A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 53, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

Claim 21. (Original) A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

Claims 22-49 (canceled)

Claims 50-51 (Not entered)

Claim 52. (Previously presented) A method of claim 8, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:1.

Claim 53. (Previously presented) A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:2.